

AperTO - Archivio Istituzionale Open Access dell'Università di Torino

Detection and dynamics of volatile/non-volatile metabolite induction in a fungal co-culture through a miniaturised MS-based metabolomic approach

This is the author's manuscript

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/1614803> since 2016-11-21T12:20:09Z

Publisher:

-

Terms of use:

Open Access

Anyone can freely access the full text of works made available as "Open Access". Works made available under a Creative Commons license can be used according to the terms and conditions of said license. Use of all other works requires consent of the right holder (author or publisher) if not exempted from copyright protection by the applicable law.

(Article begins on next page)

Detection and dynamics of volatile/non-volatile metabolite induction in fungal co-culture through a miniaturised MS-based metabolomic approach

Antonio Azzollini¹, Lorenzo Boggia², Julien Boccard¹, Barbara Sgorbini², Nicole Lecoutre³, Patrizia Rubiolo², Serge Rudaz¹, Katia Gindro³, Carlo Bicchi², Jean-Luc Wolfender¹

¹School of Pharmaceutical Sciences, University of Geneva, University of Lausanne, Quai Ernest-Ansermet 30, CH-1211 Geneva 4, Switzerland; ²Department of Drug Science and Technology, University of Turin, Via P. Giuria 9, 10125, Turin, Italy; ³Agroscope, Institute for Plant Production Sciences IPS, Mycology and Biotechnology, Route de Duiller 50, PO Box 1012, 1260 Nyon 1, Switzerland.

Microbial co-cultivation has emerged as a promising way for activating cryptic biosynthetic pathways and discovering novel antimicrobial metabolites [1]. For the success of such studies, a key element remains the development of standardized co-cultivation methods compatible with high throughput analytical procedures [2]. In our continuous studies on the dynamic stress induction of bioactive natural products in co-culture conditions, we have extended the investigations to modifications of the microbial volatile metabolome that might be of importance in the understanding of the interaction between microorganisms.

For this, an MS metabolomic strategy based on the analysis of volatile and non-volatile fractions of the fungal cultures directly grown in 20 ml vials was applied. The head space of each sample was profiled by SPME-GC-MS while the whole culture medium was analyzed by LC-HRMS after solvent extraction. This strategy was implemented for screening volatile/non-volatile metabolite inductions in an ecologically relevant fungal co-culture of *Eutypa lata* (Pers.) Tul. & C. Tul. (Diatrypaceae) and *Botryosphaeria obtusa* (Schwein.) Shoemaker (Botryosphaeriaceae), two wood decaying fungi interacting in the context of esca disease of grapevine [3]. Multivariate data analysis combining Analysis of Variance (ANOVA) and Orthogonal Partial Least Squares (OPLS) conducted to the selection of specific induced molecules related to each factor of the study. A time-series study during nine days showed characteristic metabolite induction patterns. Interesting relationships between the dynamics of volatile/non-volatile metabolite *de novo* formation and up- or down-regulation could be highlighted. Some of the induced compounds (*e.g.*, 2-nonanone) are bioactive and known to be produced by other microorganisms. The developed strategy could help elucidating the microbial inter- and intra-species communication. Moreover it could be used for efficiently identifying signaling molecules with potential antimicrobial activity.

Keywords: volatile/non-volatile metabolite induction, microbial co-cultivation, SPME-GC-MS, LC-HRMS, metabolomics

References:

- [1] Bertrand S, Bohni N, Schnee S, Schumpp O, Gindro K, Wolfender JL. Metabolite induction via microorganism co-culture: A potential way to enhance chemical diversity for drug discovery. *Biotechnol Adv* 2014; 32: 1180–1204
- [2] Bertrand S, Azzollini A, Schumpp O, Bohni N, Schrenzel J, Monod M, Gindro K, Wolfender JL. Multi-well fungal co-culture for *de novo* metabolite-induction in time-series studies based on untargeted metabolomics. *Mol BioSyst* 2014; 10: 2289–2298
- [3] Glauser G, Gindro K, Fringeli J, De Joffrey JP, Rudaz S, Wolfender JL. Differential analysis of mycoalexins in confrontation zones of grapevine fungal pathogens by ultrahigh pressure liquid chromatography/time-of-flight mass spectrometry and capillary nuclear magnetic resonance. *J Agric Food Chem* 2009; 57: 1127–1134